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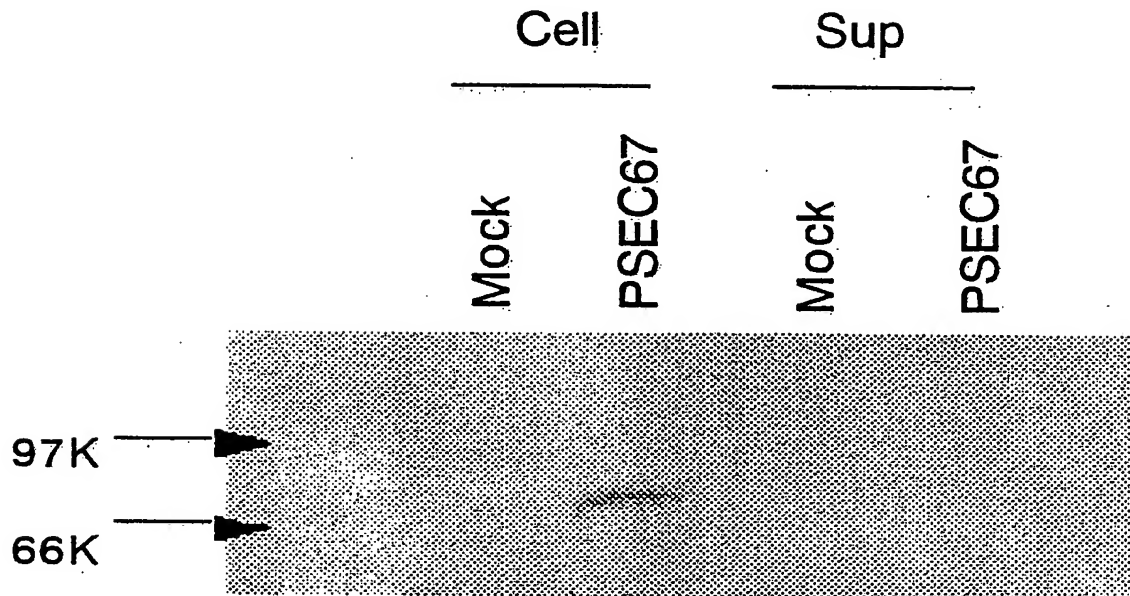
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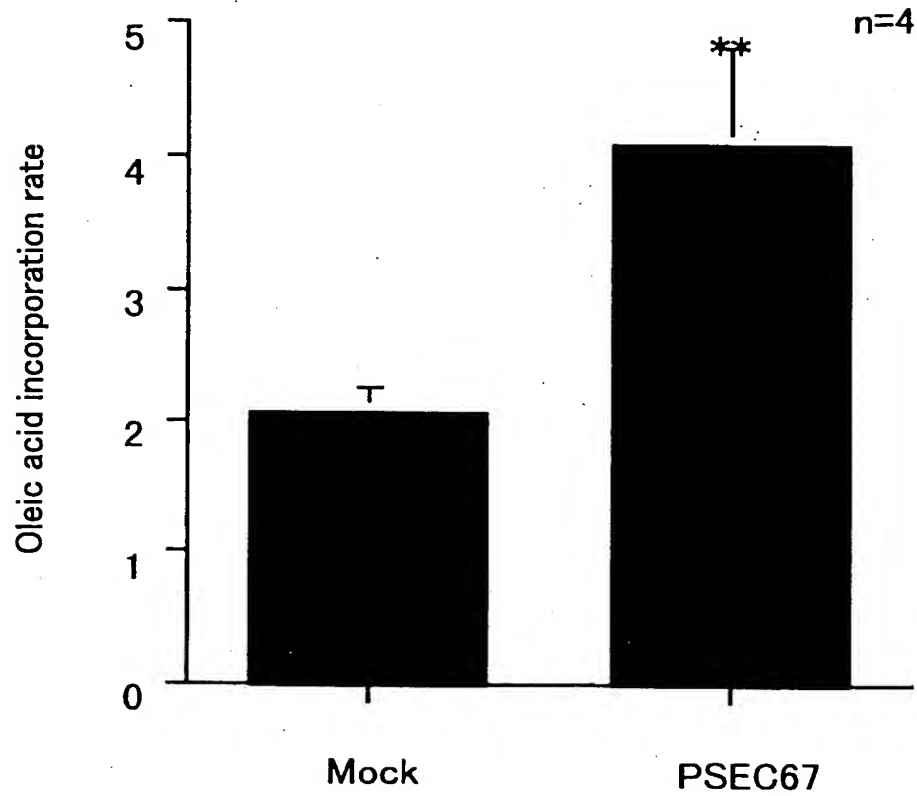
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Figure 1



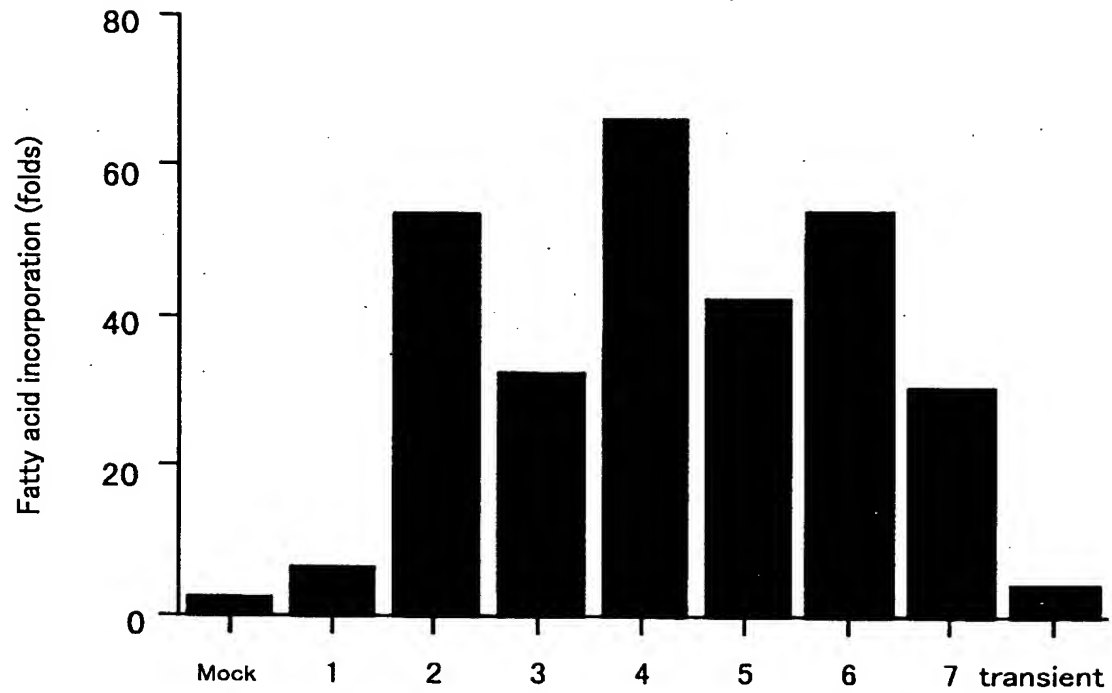
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Figure 2



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Figure 3



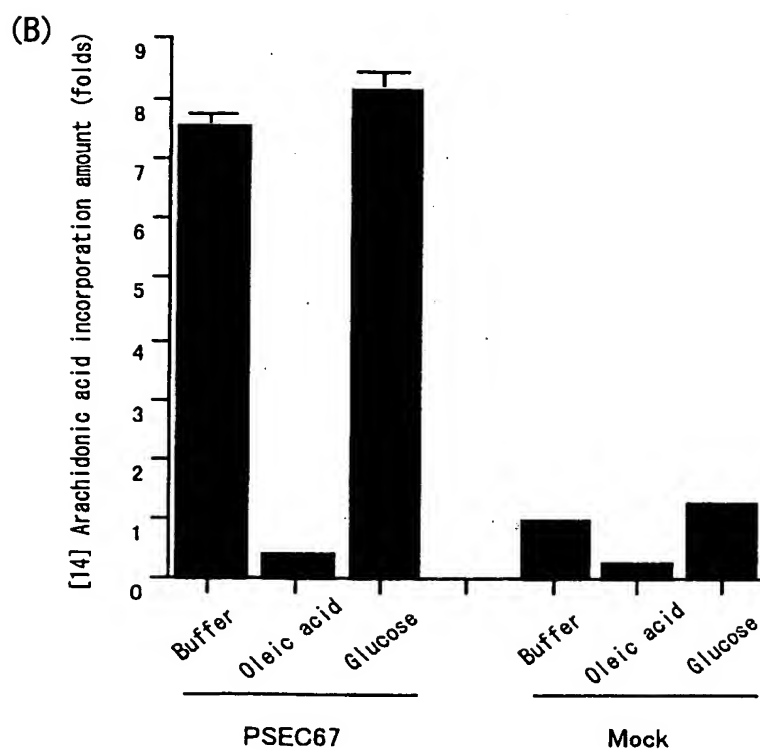
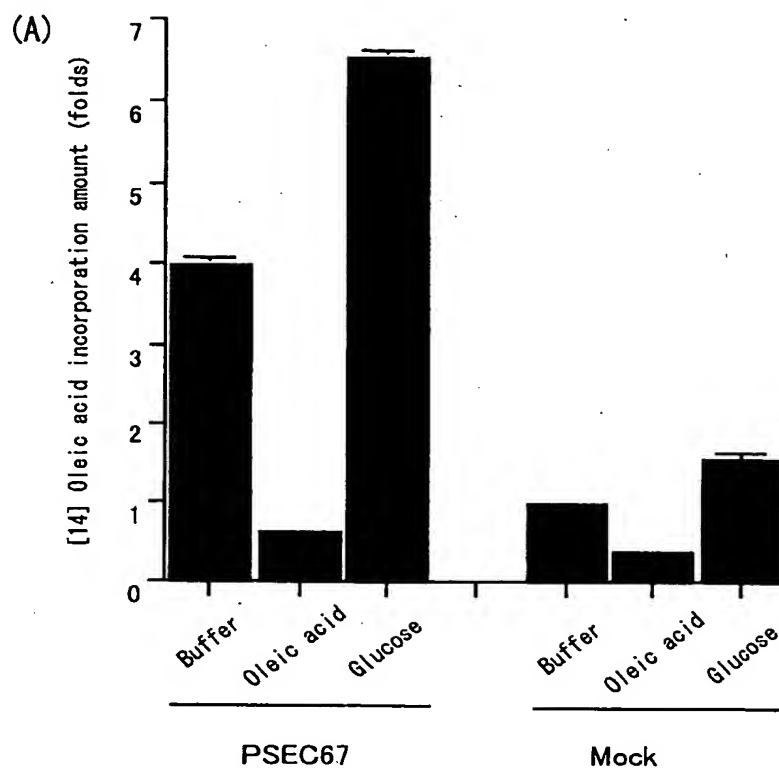
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Figure 4



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Figure 5



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Figure 6

PSEC67:	501	ACAGGGCTGCACGGCCTTC-CTACGTGCGCTAGGCTGGGACTGGGACCCGACGGCG-G	558
		AC G GC GCA GGC TT CTACG G G AGGCTG G C G GA C CGG G	
m. FATP3:	98	ACGGCGC-GCA-GCGCTTTAGCTACGG-G-AGGCTGAG-CGCGAGAGCAACCGATTG	151
PSEC67:	559	CGACAGGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCGG-GGAGCCGG-AGAT	616
		C C GCG C G GCGC G G G GA CGGG CGCGG GG C GG AG	
m. FATP3:	152	CT-C-GCGCCTTTCTGCGCGCACGGGGCTG-GACCGGGGGCGCGGAGGCTCGGGCAGGG	208
PSEC67:	617	GCAGCGGCC-GGAAG-CGG-CGCG-GAGTTTGCCGGAGGG-GACGGTGCCGCCAGAGGT	670
		GCAGC GGAAG CG CGCG G G T CCGG GG GA G GC GC AGAGG	
m. FATP3:	209	GCAGCACTGAGGAAGGCGCACGCGTGGCGCT-CGGCTGGAGATGCGGCTGCTAGAGG-	266
PSEC67:	671	GGAGGAGCGCGCGCCCTCTGTGCACTGGAGCAACTGTGGCGCTGCTCCTCCCGCTGGC	730
		GA GA CGC CCGCTCTG CACC GG GC AC GTGGCGCTGCTCCTCC GC GGC	
m. FATP3:	267	-GACGA-CGCGCGCCCTCTGTGCACCGGGCGACCGTGGCGCTGCTCCTCCAGCGGGC	324
PSEC67:	731	CCAGAGTTTCTGTGGCTCTGGTTCCGGCTGGCCAAGGCCGGCTGCGCACTGCCTTTGTG	790
		CC GA TT CT TGG T TGGTTCCG CTGGCCAA GC GGCTGCGCAC GCCTTTGTG	
m. FATP3:	325	CCGATTTCCTTTGATTGTGGTTCCGACTGGCCAAAGCTGGCTGCGCACGGCCTTTGTG	384
PSEC67:	791	CCCACCGCCCTGCGCGGGGGCCCCCTGCTGCACTGCCTCCGAGCTGCGGCGCGCGCGG	850
		CCCACGC T CGCG GG CCGCTGCTGCACTGCCTCCGAGCTGCGG GCG G GCG	
m. FATP3:	385	CCCACCGCTTTACGCGGAGGACCCCTGCTGCACTGCCTCCGAGCTGCGGTGCGAGTGCG	444
PSEC67:	851	CTGGTGCTGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCC	910
		CT GTGCTGGC CAGAGTT CTGGAGTCCCTGGAGCCGGACCTGCC GCC TGAGAGCC	
m. FATP3:	445	CTGTGCTGGCCACAGAGTTCTGGAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCC	504
PSEC67:	911	ATGGGGCTCCACCTGTGGGCTGCAGGCCAGGAACCCACCTGCTGGAATTAGCGATTTG	970
		ATGGGGCTCCACCT TGGG C GGCC G AAC A GCTGGAAT AGC ATTTG	
m. FATP3:	505	ATGGGGCTCCACCTATGGGCGACGGGCCCTGAACTAATGTAGCTGGAATCAGCAATTTG	564
PSEC67:	971	CTGGCTGAAGTGTCGCTGAAGTGGATGGGCCAGTGCCAGGATACTCTCTTCCCCCAG	1030
		CT C GAAG C G AAGTGGATG GCCAGTGCC GG TACCTCTCT CCCCCAG	
m. FATP3:	565	CTATCGGAAGCAGCAGACCAAGTGGATGAGCCAGTGCCGGGTACCTCTCTGCCCCCAG	624
PSEC67:	1031	AGCATAACAGACACGTGCCTGTACATCTTCACTCTGGCACCACGGGCCTCCCCAAGGCT	1090
		A CATAA GACAC TGCTGTACATCTTCACTCTGGCAC AC GGCT CCAAGGCT	
m. FATP3:	625	AACATAATGGACACCTGCCTGTACATCTTCACTCTGGCACTACTGGCTGCCAAGGCT	684
PSEC67:	1091	GCTCGGATCAGTCATCTGAAGATCCTGCAATGCCAGGGCTTCTATCAGCTGTGTGGTGTC	1150
		GCTCG ATCAGTCATCTGAAG T CT CA TGCCAGGG TTCTA CA CTGTGTGG GTC	
m. FATP3:	685	GCTCGAATCAGTCATCTGAAGGTTCTACAGTGCCAGGGATTCTACCATCTGTGTGGAGTC	744
PSEC67:	1151	CACCAGGAAGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGGTCCCTGCTG	1210
		CACCAGGA GA GTGATCTACCTCGC CTCCCACT TACCACATGTC GG TCCCT CTG	
m. FATP3:	745	CACCAGGAGGACGTGATCTACCTCGCACTCCCACTGTACCACATGTCTGGTCCCTTCTG	804
PSEC67:	1211	GGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTGGTGCTGAAATCCAAGTTCTCGGCT	1270
		GGCAT GTGGCTGC TGGGCATTGGGGCCAC GTGGTGCTGAAA CCAAGTTCTC GCT	
m. FATP3:	805	GGCATTGTGGGCTGCTTGGGCATTGGGGCCACCGTGGTGCTGAAACCAAGTTCTCAGCT	864

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Figure 7

PSEC67: 1271	GGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCAGTACATTGGGGAG	1330
	G CAGTTCTGGGA GATTGCCAG A CACAGGGTGAC GTGTTCCAGTACATTGGGGAG	
m. FATP3: 865	AGCCAGTTCTGGGAAGATTGCCAGAAACACAGGGTGACAGTGTTCAGTACATTGGGGAG	924
PSEC67: 1331	CTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAGAACGTGGCCATAAGGTCCGG	1390
	TGTGCCGATACCT GTCAACCAGCCCCGAGCAAGGCAG TG CCATAAGGT CG	
m. FATP3: 925	TTGTGCCGATACCTCGTCAACCAGCCCCGAGCAAGGCAGAGTTTGACCATAAGGTGCGC	984
PSEC67: 1391	CTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGTTTGTGCGGCGCTTCGGG	1450
	TGGCAGTGGGCAG GGG TGCGCCAG ACCTGGGAGCGTTT TGCGCG TT GG	
m. FATP3: 985	TTGGCAGTGGGCAGTGGGTTGCGCCAGACACCTGGGAGCGTTTCTGCGGCGATTGGA	1044
PSEC67: 1451	CCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCATCAACTAC	1510
	CC CTGCAG T CTGGAGAC TATGG TGACAGAGGGCAACGT GC AC TCAA TAC	
m. FATP3:1045	CCTCTGCAGATACTGGAGACGTATGGCATGACAGAGGGCAACGTAGCTACGTTCAATTAC	1104
PSEC67: 1511	ACAGGACAGCGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGCATATCTTCCCTTC	1570
	ACAGGAC GC GGG GC GTGGGGCG GCTTCTGGCTTTACAAGCA ATCTTCCCTTC	
m. FATP3:1105	ACAGGACGGCAGGGTGCAAGTGGGGCGAGCTTCTGGCTTTACAAGCACATCTTCCCTTC	1164
PSEC67: 1571	TCCTTGATTGCTATGATGTCAACACAGGAGAGCCAATTGCGGACCCCGAGGGGCACTGT	1630
	TCCTTGATTG TA GATGTCA ACAGG GAGCC ATTCGG A CCCAGGGGCACTG	
m. FATP3:1165	TCCTTGATTGATACGATGTCTATGACAGGGAGCGCTATTCGGAATGCCAGGGGCACTGC	1224
PSEC67: 1631	ATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCA	1690
	ATG CCACATCTCCAGGTGAGCCAGG CT CTGGTGGCCCC GT AGCCAGCAGTCCCC	
m. FATP3:1225	ATGACCACATCTCCAGGTGAGCCAGGCGTACTGGTGGCCCCAGTGAGCCAGCAGTCCCC	1284
PSEC67: 1691	TTCTTGGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGGAAGTTGCTAAAGGATGTCTTC	1750
	TTCTTGGGCTATGCTGG G CC GAGCTGGCC AGG AAG TGCT AAGGATGTCTTC	
m. FATP3:1285	TTCTTGGGCTATGCTGGGGCTCCGAGCTGGCCAAGGACAAGCTGCTGAAGGATGTCTTC	1344
PSEC67: 1751	CGGCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAAGGTTTT	1810
	GG CTGGGGA GTTTTCTTCAA ACTGGGACCT TGGTCTG GATGA CAAGG TTT	
m. FATP3:1345	TGGTCTGGGGACGTTTTCTTCAATACTGGGGACCTCTTGGTCTGTGATGAGCAAGGCTTT	1404
PSEC67: 1811	CTCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGAGAAATGTGGCCACA	1870
	CT C CTCCA GATCGTACTGGAGACACC TCAGGTGGAAGGG GAGAAATGTGGCCACA	
m. FATP3:1405	CTTCACTTCCAGATCGTACTGGAGACACCATCAGGTGGAAGGGAGAGAAATGTGGCCACA	1464
PSEC67: 1871	ACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGA	1930
	AC GA GTGGC GAGGTCTT GAG CCT GA TT CTCAGGAGGTGAAC TCTATGGA	
m. FATP3:1465	ACTGAAGTGGCTGAGGTCTTGAGACCCCTGGACTTCCTTCAGGAGGTGAACATCTATGGA	1524
PSEC67: 1931	GTCAGTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC	1990
	GTCAC GTGCCAGGGCA GAAGGCAGGGC GG ATGGC GCC T G TCTGCG CCCCC	
m. FATP3:1525	GTCACGGTGGCAGGGCAAGAAGGCAGGGCAGGCATGGCGGCTTGGCTCTGCGGCCCCG	1584
PSEC67: 1991	CAAGCTTTGGACCTTATGCAGCTCTACACCCAGTGTCTGAGAACTTGCCACCTTATGCC	2050
	CA GCT TG ACCT TGCAGCTCTACA CCA GT TCTGAGAACTTGCCACC TATGCC	
m. FATP3:1585	CAGGCTCTGAACCTGGTGCAGCTCTACAGCCATGTTTCTGAGAACTTGCCACCGTATGCC	1644
PSEC67: 2051	CGGCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAG	2110
	CG CC CG TT CTCAGGCTCCAGGA TCTTTGGCCAC AC GAGACCTTCAAACAGCAG	
m. FATP3:1645	CGACCTCGGTTTCTCAGGCTCCAGGAATCTTTGGCCACTACTGAGACCTTCAAACAGCAG	1704



Title: FATTY ACID TRANSPORTER  
PROTEINS AND THE GENES ENCODING  
THE PROTEINS

Inventor(s): MORIKAWA Noriyuki et al.  
Attorney Docket No.: 084335-0154

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Figure 8

PSEC67: 2111	AAAGTTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCCTGTCTGACCCACTGTACGTT	2170
	AA GTT GGATGGC AATGAGGGCTT GACCCCAG CTGTCTGACCCACT TA GTT	
m. FATP3:1705	AAGGTTAGGATGGCCAATGAGGGCTTTGACCCCAGTGACTGTCTGACCCACTCTATGTT	1764
PSEC67: 2171	CTGGACCAGGCTGTAGGTGCCTACCTGCCCCCTCACAACCTGCCCGGTACAGCGCCCTCCTG	2230
	CTGGACCA G T TAGG GCCTACCTGCCCCCTCACA CTGCCCGGTACAG GCCCTCCTG	
m. FATP3:1765	CTGGACCAAGATATAGGGGCTACCTGCCCCCTCACACCTGCCCGGTACAGTGCCCTCCTG	1824
PSEC67: 2231	GCAGGAAACCTTCGAATCTGA	2251
	C GGA ACCTTCGAATCTGA	
m. FATP3:1825	TCTGGAGACCTTCGAATCTGA	1845

PSEC67:	61'	PLLLKLHLWPLRLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAE	*****. *. *****
m. FATP3:	1"		AAADPESESGCSLAWRLAY
PSEC67:	121'	LAQQRAAHTFLIHGSRRFYSYSEAESNRAARAFLRALGWDWGPDDGSDGECSAGEGERA	**.....*****.****.***** ***** **.
m. FATP3:	21"	LAREQPTHTFLIHGAQRFYSYAEAESNRIRARAFRLARGWTGRRGSGR—GSTEEGARV	***. *. *... **..**.*.
PSEC67:	181'	APGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLR	** *** .*** *. *. **.
m. FATP3:	79"	APPAGD—AAAR—GTTAPPLAPGATVALLLPAGPDFLWIWFGGLAKAGLR	*****.***.*****
PSEC67:	241'	TAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG	*****.*****.*****.***.*. **
m. FATP3:	125"	TAFVPTALRRGPLLHCLRSCGASALVLAPEFLESLEPDLPALRAMGLHLWATGPETNVAG	
PSEC67:	301'	ISDLLAEVSAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQ	**.*.*...**.*****.***.* *****.*****.
m. FATP3:	185"	ISNLLSEAADQVDEPVPGYLSAPQNMIDTCLYIFTSGTTGLPKAARISHLKVLQCQGFYH	*****.
PSEC67:	361'	LCGVHQEDVIYLALPLYHMSGSLGIVGCMGIGATVVLKSKFSAGQFWEDCQQRHVTVFQ	*****.*****.*****.***.***.*****
m. FATP3:	245"	LCGVHQEDVIYLALPLYHMSGSLGIVGCLGIGATVVLKPKFSASQFWDDCQKHRVTVFQ	
PSEC67:	421'	YIGELCRYLVNQPPSKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNA	*****.*****.*****.*****.*****
m. FATP3:	305"	YIGELCRYLVNQPPSKAEFDHKVR LAVGSGLRPDTWERFLRRFGPLQILETYGMTEGNA	
PSEC67:	481'	TINYTGQRGAVGRASWLYKHIFPFSLI RYDVTTGEP IRDPQGHCMATSPGEPGLLVAPVS	*.***.*.***** *****.*****.*****
m. FATP3:	365"	TFNYTGQRGAVGRASWLYKHIFPFSLI RYDVTTGEP IRNAQGHCMITSPGEPGLLVAPVS	
PSEC67:	541'	QQSPFLGYAGGPPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGF LRFH DRTGDTFRWKGE	*****.***.*.*****.*****.*****.*****
m. FATP3:	425"	QQSPFLGYAGAPELAKDKLLKDVFWSGDVFFNTGDLLVCDEQGF LHFH DRTGDTIRWKGE	
PSEC67:	601'	NVATTEVAEVFEALDFLQEVN VYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSEN	*****.*.*****.*****.***.*.***.*****
m. FATP3:	485"	NVATTEVAEVLETDLFLQEVNIYGVTVPGHEGRAGMAALALRPPQALNLVQLYSHVSEN	
PSEC67:	661'	PPYARPRFLRLQESLATTETFKQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARY	*****.*****.*****.*****.*****.***
m. FATP3:	545"	PPYARPRFLRLQESLATTETFKQKVRMANEGFDP SVLSDPLYVLDQDIGAYLPLTPARY	
PSEC67:	721'	SALLAGNLRI	***.*.***
m. FATP3:	605"	SALLSGDLRI	

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Figure 10

PSEC67:	61'	PLLLKLHLWPQLRWLPADLAFVRLCCKRALRARALAAAAADPEGPEGGCSLAWRLAE
acyl CoA:	1"	MLSAIYTVLA
PSEC67:	121'	LAQQRAAHTFLIHGSRFFSYSEAERESNRAARAFLRALGWDWGPDDGDSGEGSAGEGERA
acyl CoA:	11"	GLLFLPLLVLNCCPYFFQDIGYFLKVAAGVRRVRSYGQRRPARTILRAFLEKARQTPHKP
PSEC67:	181'	APGAGDAAAGSGAEFAGGDGAARGGGAAPLSPGATVALLLPAGPEFLWLWFLGAKAGLR
acyl CoA:	71"	FLLFRDETLTYAQVDRRSNQVARALHDHLGLRQGDCAVLLMGNEPAYVWLWLGLVKLGCA
PSEC67:	241'	TAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG
acyl CoA:	131"	MACLNYNIRAKSLLHCFQCCGAKVLLVSPELQAAVEEILPSLKDDVSIYYVSRTSNTDG
PSEC67:	301'	ISDLLAEVSAEVDGPVPGYLSSPQSITDTCL <u>YIFTS GTTGLP</u> KAARISHLKILQCQGFYQ
acyl CoA:	191"	IDSFLDKVDEVSTEPIPESEWRSEVTFSTPAL <u>YIYTS GTTGLP</u> KAAMITHQRIWYGTGLTF
PSEC67:	361'	LCGVHQEDVIYLALPLYHMSGSLGIVGCMGIGATVVLKSKFSAGQFVEDCQQHRVTVFQ
acyl CoA:	251"	VSGLKADDVIYITLPHYHSAALLIGIHGCIVAGATLALRTKFSASQFWDCCRKYNTVIQ
PSEC67:	421'	YIGELCRYLVNQPPSKAERGHKVR LAVSGSLRPDTWERFVRRFGPLQVLETYGLTEGNVA
acyl CoA:	311"	YIGELLRYLCNSPQKPNDRDHKVR LALGNLGRGDVWRQFVKRFGDICIYEFYAATEGNIG
PSEC67:	481'	TINYTGQRGAVGRASWLYKHIFPFS LIRYDVTTGEP IRDPQGHCMATSPGEPGLLVAPVS
acyl CoA:	371"	FMNYARKVGAVGRVNYLQKKIITYDLIKYDVEKDEPVRDENGVCVRVPKGEVGLLVCKIT
PSEC67:	541'	QQSPFLGYAGGP ELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGF LR <u>FH DRTGDTFRWKGE</u>
acyl CoA:	431"	QLTPFNQYAGAKAQTEKKLRDVF KKGDL YFNSGDLLMVDHENFIY <u>FH DRTGDTFRWKGE</u>
PSEC67:	601'	<u>NVATTEV</u> AEVFEALDFLQEVN VYGVTVP GHEGRAGMAALVLRPPHALDLMQLYTHVSEN L
acyl CoA:	491"	<u>NVATTEV</u> ADTVGLVDFVQEVN VYGVHVPDHEGRIGMASIKMKENHEFDGKKLFQHIADYL
PSEC67:	661'	PPYARPRFLRLQESLATTETFKQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARY
acyl CoA:	551"	PSYARPRFLRIQDTIEITGTGFKHRKMTLVEEGFNPAVIKDALYFLDDTAKMYVPMTEDIY
PSEC67:	721'	SALLAGNLRI
acyl CoA:	611"	NAISAKTLKL